

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Dana-Farber, Corporation  
KOLODNER, Richard  
WINAND, Nena
- (ii) TITLE OF THE INVENTION: A Method for Detection of  
Alteration in MSH5
- (iii) NUMBER OF SEQUENCES: 104
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
  - (B) STREET: 130 Water Street
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 60/051,686
  - (B) FILING DATE: 03-JUL-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Eisenstein, Ronald I
  - (B) REGISTRATION NUMBER: 30,628
  - (C) REFERENCE/DOCKET NUMBER: 157/47483-PCT
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 617-523-3400
  - (B) TELEFAX: 617-523-6440
  - (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2900 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCTCCTTTT	GCAGGCTCGT	GGCGGTCCGT	CAGCGGGGCG	TTCTCCCACC	TGTAGCGACT	60
CAGGTTACTG	AAAAGGCGGG	AAAACGCTGC	GATGGCGGCA	GCTGGGGGAG	GAGGAAGATA	120
AGCGCGTGAG	GCTGGGGTCC	TGGCGCGTGG	TTGGCAGAGG	CAGAGACATA	AGACGTGCAC	180
GACTCGCCCC	ACAGGGCCTT	CAGACCCCTT	CTTTCCAAAG	GAGCCTCCAA	GCTCATGGCC	240
TCCTTAGGAG	CGAACCCAAG	GAGGACACCG	CAGGGACCGA	GACCTGGGGC	GGCCTCCTCC	300
GGTTTCCCCA	GCCCCGCCCC	AGTGCCGGGC	CCCAGGGAGG	CCGAGGAGGA	GGAAGTCGAG	360
GAGGAGGAGG	AGCTGGCCGA	GATCCATCTG	TGTGTGCTGT	GGAATTCAGG	ATACTTGGGC	420
ATTGCCTACT	ATGATACTAG	TGACTCCACT	ATCCAATTCA	TGCCAGATGC	CCCAGACCAC	480
GAGAGCCTCA	AGCTTCTCCA	GAGAGTTCTG	GATGAGATCA	ATCCCCAGTC	TGTTGTTACG	540
AGTGCCAAAC	AGGATGAGAA	TATGACTCGA	TTTCTGGGAA	AGCTTGCCCTC	CCAGGAGCAC	600
AGAGAGCCTA	AAAGACCTGA	AATCATATTT	TTGCCAAGTG	TGGATTTTGG	TCTGGAGATA	660
AGCAAACAAC	GCCTCCTTTC	TGGAAACTAC	TCCTTCATCC	CAGACGCCAT	GACTGCCACT	720
GAGAAAATCC	TCTTCCTCTC	TTCCATTATT	CCCTTTGACT	GCCTCCTCAC	AGTTCGAGCA	780
CTTGGAGGGC	TGCTGAAGTT	CCTGGGTCTG	AGAAGAATCG	GGGTTGAACT	GGAAGACTAT	840
AATGTCAGCG	TCCCCATCCT	GGGCTTTAAG	AAATTTATGT	TGACTCATCT	GGTGAACATA	900
GATCAAGACA	CTTACAGTGT	TCTACAGATT	TTTAAGAGTG	AGTCTCACCC	CTCAGTGTAC	960
AAAGTGGCCA	GTGGACTGAA	GGAGGGGCTC	AGCCTCTTTG	GAATCCTCAA	CAGATGCCAC	1020
TGTAAGTGGG	GAGAGAAGCT	GCTCAGGCTA	TGGTTACAC	GTCCGACTCA	TGACCTGGGG	1080
GAGCTCAGTT	CTCGTCTGGA	CGTCATTGAG	TTTTTTCTGC	TGCCCCAGAA	TCTGGACATG	1140
GCTCAGATGC	TGCATCGGCT	CCTGGGTCTC	ATCAAGAACG	TGCCTTTGAT	TCTGAAACGC	1200
ATGAAGTTGT	CCCACACCAA	GGTCAGCGAG	TGGCAGGTTT	TCTACAAGAC	TGTGTACAGT	1260
GCCCTGGGCC	TGAGGGATGC	CTGCCGCTCC	CTGCCGCGAT	CCATCCAGCT	CTTTGGGGAC	1320
ATTGCCCAAAG	AGTTCTCTGA	TGACCTGCAC	CATATCGCCA	GCCTCATTGG	GAAAGTAGTG	1380
GACTTTGAGG	GCAGCCTTGC	TGAAAAATCG	TTACAGTCTC	TCCCCAACAT	AGATCCTGAA	1440
ATTGATGAGA	AAAAGCGAAG	ACTGATGGGA	CTTCCAGTTT	TCCTTACTGA	GGTTGCCCGC	1500
AAGGAGCTGG	AGAATCTGGA	CTCCCGTATT	CCTTCATGCA	GTGTCTATCT	CATCCCTCTG	1560
ATTGGCTTCC	TTCTTTCTAT	TCCCCGCTTG	CCTTCCATGG	TAGAGGCCAG	TGACTTTGAG	1620
ATTAATGGAC	TGGACTTCAT	GTTTCTCTCA	GAGGAGAAGC	TGCACTATCG	TAGTGCCCGA	1680
ACCAAGGAGC	TGGATGCATT	GCTGGGGGAG	CTGCACTGCG	AGATCCGGGA	CCAGGAGACG	1740
CTGCTGATGT	ACCAGCTACA	GTGCCAGGTG	CTGGCACGAG	CAGCTGTCTT	AACCCGAGTA	1800
TTGGACCTTG	CCTCCCGCCT	GGACGTCCGT	CTGGCTCTTG	CCAGTGCTGC	CCGGGACTAT	1860
GGCTACTCAA	GGCCGCGTTA	CTCCCCACAA	GTCTTTGGGG	TACGAATCCA	GAATGGCAGA	1920
CATCCTCTGA	TGGAACCTCT	TGCCCCGAAC	TTTGTGCCCA	ACTCCACAGA	ATGTGGTGGG	1980
GACAAAGGGA	GGGTCAAAGT	CATCACTGGA	CCCAACTCAT	CAGGGAAGAG	CATATACCTC	2040
AAACAGGTAG	GCTTGATCAC	ATTCATGGCC	CTGGTAGGCA	GCTTTGTGCC	AGCAGAGGAG	2100
GCCGAAATTG	GGGCAGTAGA	CGCCATCTTC	ACACGAATTG	ATAGCTGCGA	ATCCATCTCC	2160
CTTGGCCTCT	CCACCTTCAT	GATCGACCTC	AACCAGGTGG	CGAAAGCAGT	GAACAATGCC	2220
ACTGCACAGT	CGCTGGTCTT	TATTGATGAA	TTTGAAAGG	GAACCAACAC	GGTGGATGGG	2280
CTCGCGCTTC	TGGCCGCTGT	GCTCCGACAC	TGGCTGGCAC	GTGGACCCAC	ATGCCCCCAC	2340
ATCTTTGTGG	CCACCAACTT	TCTGAGCCTT	GTTTCAGCTAC	AACTGCTGCC	ACAAGGGCCC	2400
CTGGTGCAGT	ATTTGACCAT	GGAGACCTGT	GAGGATGGCA	ACGATCTTGT	CTTCTTCTAT	2460
CAGGTTTGGC	AAGGTGTTGC	GAAGGCCAGC	CATGCCTCCC	ACACAGCTGC	CCAGGCTGGG	2520
CTTCCTGACA	AGCTTGTGGC	TCGTGGCAAG	GAGGTCTCAG	ATTTGATCCG	CAGTGGAATA	2580
CCCATCAAGC	CTGTCAAGGA	TTTGCTAAAG	AAGAACCAAA	TGAAAATTG	CCAGACATTA	2640

GTGGATAAGT	TTATGAAACT	GGATTTGGAA	GATCCTAACC	TGGACTTGAA	CGTTTTTCATG	2700
AGCCAGGAAG	TGCTGCCTGC	TGCCACCAGC	ATCCTCTGAG	AGTCCTTCCA	GTGTCCCTCCC	2760
CAGCCTCCTG	AGACTCCGGT	GGGCTGCCAT	GCCCTCTTTG	TTTCCTTATC	TCCCTCAGAC	2820
GCAGAGTTTT	TAGTTTCTCT	AGAAATTTTG	TTTCATATTA	GGAATAAAGT	TTATTTTGAA	2880
GAATAAAGT	AAAAAATAAA					2900

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Ala	Ser	Leu	Gly 5	Ala	Asn	Pro	Arg	Arg 10	Thr	Pro	Gln	Gly	Pro 15	Arg
Pro	Gly	Ala	Ala	Ser	Ser	Gly	Phe	Pro	Ser	Pro	Ala	Pro	Val	Pro	Gly
			20					25					30		
Pro	Arg	Glu	Ala	Glu	Glu	Glu	Glu	Val	Glu	Glu	Glu	Glu	Glu	Leu	Ala
		35					40					45			
Glu	Ile	His	Leu	Cys	Val	Leu	Trp	Asn	Ser	Gly	Tyr	Leu	Gly	Ile	Ala
	50					55					60				
Tyr	Tyr	Asp	Thr	Ser	Asp	Ser	Thr	Ile	His	Phe	Met	Pro	Asp	Ala	Pro
65					70					75					80
Asp	His	Glu	Ser	Leu	Lys	Leu	Leu	Gln	Arg	Val	Leu	Asp	Glu	Ile	Asn
				85					90					95	
Pro	Gln	Ser	Val	Val	Thr	Ser	Ala	Lys	Gln	Asp	Glu	Asn	Met	Thr	Arg
			100					105					110		
Phe	Leu	Gly	Lys	Leu	Ala	Ser	Gln	Glu	His	Arg	Glu	Pro	Lys	Arg	Pro
		115					120					125			
Glu	Ile	Ile	Phe	Leu	Pro	Ser	Val	Asp	Phe	Gly	Leu	Glu	Ile	Ser	Lys
	130					135					140				
Gln	Arg	Leu	Leu	Ser	Gly	Asn	Tyr	Ser	Phe	Ile	Pro	Asp	Ala	Met	Thr
145					150					155					160
Ala	Thr	Glu	Lys	Ile	Leu	Phe	Leu	Ser	Ser	Ile	Ile	Pro	Phe	Asp	Cys
				165					170					175	
Leu	Leu	Thr	Val	Arg	Ala	Leu	Gly	Gly	Leu	Leu	Lys	Phe	Leu	Gly	Arg
			180					185					190		
Arg	Arg	Ile	Gly	Val	Glu	Leu	Glu	Asp	Tyr	Asn	Val	Ser	Val	Pro	Ile
		195					200					205			
Leu	Gly	Phe	Lys	Lys	Phe	Met	Leu	Thr	His	Leu	Val	Asn	Ile	Asp	Gln
	210					215					220				
Asp	Thr	Tyr	Ser	Val	Leu	Gln	Ile	Phe	Lys	Ser	Glu	Ser	His	Pro	Ser
225					230					235					240
Val	Tyr	Lys	Val	Ala	Ser	Gly	Leu	Lys	Glu	Gly	Leu	Ser	Leu	Phe	Gly
				245					250					255	
Ile	Leu	Asn	Arg	Cys	His	Cys	Lys	Trp	Gly	Glu	Lys	Leu	Leu	Arg	Leu
		260						265					270		
Trp	Phe	Thr	Arg	Pro	Thr	His	Asp	Leu	Gly	Glu	Leu	Ser	Ser	Arg	Leu
		275					280					285			

Asp Val Ile Gln Phe Phe Leu Leu Pro Gln Asn Leu Asp Met Ala Gln  
 290 295 300  
 Met Leu His Arg Leu Leu Gly His Ile Lys Asn Val Pro Leu Ile Leu  
 305 310 315 320  
 Lys Arg Met Lys Leu Ser His Thr Lys Val Ser Asp Trp Gln Val Leu  
 325 330 335  
 Tyr Lys Thr Val Tyr Ser Ala Leu Gly Leu Arg Asp Ala Cys Arg Ser  
 340 345 350  
 Leu Pro Gln Ser Ile Gln Leu Phe Arg Asp Ile Ala Gln Glu Phe Ser  
 355 360 365  
 Asp Asp Leu His His Ile Ala Ser Leu Ile Gly Lys Val Val Asp Phe  
 370 375 380  
 Glu Gly Ser Leu Ala Glu Asn Arg Phe Thr Val Leu Pro Asn Ile Asp  
 385 390 395 400  
 Pro Glu Ile Asp Glu Lys Lys Arg Arg Leu Met Gly Leu Pro Ser Phe  
 405 410 415  
 Leu Thr Glu Val Ala Arg Lys Glu Leu Glu Asn Leu Asp Ser Arg Ile  
 420 425 430  
 Pro Ser Cys Ser Val Ile Tyr Ile Pro Leu Ile Gly Phe Leu Leu Ser  
 435 440 445  
 Ile Pro Arg Leu Pro Ser Met Val Glu Ala Ser Asp Phe Glu Ile Asn  
 450 455 460  
 Gly Leu Asp Phe Met Phe Leu Ser Glu Glu Lys Leu His Tyr Arg Ser  
 465 470 475 480  
 Ala Arg Thr Lys Glu Leu Asp Ala Leu Leu Gly Asp Leu His Cys Glu  
 485 490 495  
 Ile Arg Asp Gln Glu Thr Leu Leu Met Tyr Gln Leu Gln Cys Gln Val  
 500 505 510  
 Leu Ala Arg Ala Ala Val Leu Thr Arg Val Leu Asp Leu Ala Ser Arg  
 515 520 525  
 Leu Asp Val Leu Leu Ala Leu Ala Ser Ala Ala Arg Asp Tyr Gly Tyr  
 530 535 540  
 Ser Arg Pro Arg Tyr Ser Pro Gln Val Leu Gly Val Arg Ile Gln Asn  
 545 550 555 560  
 Gly Arg His Pro Leu Met Glu Leu Cys Ala Arg Thr Phe Val Pro Asn  
 565 570 575  
 Ser Thr Glu Cys Gly Gly Asp Lys Gly Arg Val Lys Val Ile Thr Gly  
 580 585 590  
 Pro Asn Ser Ser Gly Lys Ser Ile Tyr Leu Lys Gln Val Gly Leu Ile  
 595 600 605  
 Thr Phe Met Ala Leu Val Gly Ser Phe Val Pro Ala Glu Glu Ala Glu  
 610 615 620  
 Ile Gly Ala Val Asp Ala Ile Phe Thr Arg Ile His Ser Cys Glu Ser  
 625 630 635 640  
 Ile Ser Leu Gly Leu Ser Thr Phe Met Ile Asp Leu Asn Gln Val Ala  
 645 650 655  
 Lys Ala Val Asn Asn Ala Thr Ala Gln Ser Leu Val Leu Ile Asp Glu  
 660 665 670  
 Phe Gly Lys Gly Thr Asn Thr Val Asp Gly Leu Ala Leu Leu Ala Ala  
 675 680 685  
 Val Leu Arg His Trp Leu Ala Arg Gly Pro Thr Cys Pro His Ile Phe  
 690 695 700  
 Val Ala Thr Asn Phe Leu Ser Leu Val Gln Leu Gln Leu Leu Pro Gln

0047022460

705		710		715		720									
Gly	Pro	Leu	Val	Gln	Tyr	Leu	Thr	Met	Glu	Thr	Cys	Glu	Asp	Gly	Asn
				725					730					735	
Asp	Leu	Val	Phe	Phe	Tyr	Gln	Val	Cys	Glu	Gly	Val	Ala	Lys	Ala	Ser
			740					745					750		
His	Ala	Ser	His	Thr	Ala	Ala	Gln	Ala	Gly	Leu	Pro	Asp	Lys	Leu	Val
		755					760					765			
Ala	Arg	Gly	Lys	Glu	Val	Ser	Asp	Leu	Ile	Arg	Ser	Gly	Lys	Pro	Ile
	770					775					780				
Lys	Pro	Val	Lys	Asp	Leu	Leu	Lys	Lys	Asn	Gln	Met	Glu	Asn	Cys	Gln
785					790					795					800
Thr	Leu	Val	Asp	Lys	Phe	Met	Lys	Leu	Asp	Leu	Glu	Asp	Pro	Asn	Leu
			805						810					815	
Asp	Leu	Asn	Val	Phe	Met	Ser	Gln	Glu	Val	Leu	Pro	Ala	Ala	Thr	Ser
			820					825					830		
Ile	Leu														

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCCAAAGGG TAACCTCCGC GTGACAGAA

29

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGCCGAGG TCTCTGAGGG GAGTAGAAA

29

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCAGAGAGG TGGGGATGGA ACCATGAAT

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAAAGCTTGG TAAGGACTTG GTAAAGGAT

29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGGATTTTGG TATCTCCTTC CTTTGTGCTT

29

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCCTCACAG TGAGATTGGT CCTGGGGGA

29

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09470276 13239  
652221 9220450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATTTATGTTG TAGGTGATTC ACCCCAACC

29

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CACTTACAGG TAAAGAGGTG GAGGCATGC

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCTCTTTGG TAGGTGTGCC CCATCCCTC

29

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTGCTCAGG TGAGTGGGTC CCACACATA

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACGTGCCTG TGAGCCCAGG GTGGAGGGC

29

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCTACAAGG TAAGGCCTTC CTTCTTGAA

29

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGAAAGTAG TGAGTAGAAG GAAAAAGGG

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTGATGAGAG TGAGTGTGG GTGTGGATG

29

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:



ATCCCTCTGG TGAGGGCAGG AGAGTGGGT

29

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GACTTCATGG TAAGACCCTC AACCTCTGT

29

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGATCCGGGG TGAGGAAAAG CCAGAGGTT

29

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATGGCAGG TAAGAATAGA GGCGGGTGG

29

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCAAACAGG TGAGGAGAAG CCCTGCAGC

29

662227 9202460

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCAACCAGG TCAAAGGGAA CAAAGGGAG

29

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACCAACACGG TGAGGGGAGA AACTGATGA

29

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGTATTTGG TGAGGAGACC AATCTAGCT

29

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGCAAGGAGG TGATGAGATC CAAATGTGC

29

66222T 82202450

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATGGAAAAG TCGTATATG GCCCCAGT

29

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTCACTTTTT GCATCCGAG AGCCTCAA

29

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTTCTTCCT TGCTGGACAG ATCCATCTG

29

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCTCTGTT CTCCTTCCAG TTCTGGATG

29

## (2) INFORMATION FOR SEQ ID NO:30:

00442361329

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTTCTTTCC TCCCCACAG CCTCCCAGG

29

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGCTTGCCCTC CCTCAAATAG GTCTGGAGA

29

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CACTGCTGAT CCCCTCCCAG GTTCGAGCA

29

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTTTGTTTT CTGTCCTCAG GACTCATCT

29

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCTCCATTTC TCCTCGACAG TGTTCTACA

29

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCTGCCTTAT CCCTCACAAG AATCCTCAA

29

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACCCAAACCC TCACTTCCAG GCTATGGTT

29

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTAACCTTGT CTGACTGTAG TTGATTCTG

29

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTGTGTT TCTCTCACAG ACTGTGTAC

29

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGTACTT ATCTCCTCAG GTGGACTTT

29

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTGTCTTCC ACCCTCGTAG AAAAGCGAA

29

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTCCTCTTTA CTCTCCCCAG ATTGGCTTC

29

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTGAACCC CTGTACCCAG TTTCTCTCA

29

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCTTCCTCAC CCACTCCCAG ACCAGGAGA

29

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGCCTCTCCG CCCACTGCAG ACATCCTCT

29

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTGTCTCCTT CCCTATTCAG GTAGGCTTG

29

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTCCACCTTA TACCCAGCAG GTGGCGAAA

29

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AACCTCTGCC CTCTTTGCAG GTGGATGGG

29

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTCTTTTATT CTCTTTTAAG ACCATGGAG

29

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CACCTTCTTG CTTGTCCTAG GTCTCAGAT

29

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGATTTTCTC TCTTCTTCAG TTGCCAGAC

29

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GAATGGCAGA CATCCTCTGA

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGTATATGCT CTTCCCTGAT GA

22

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCTTGGGGC	GGTTGGTCAG	GGAGGTGGAT	CGTCGCGGCT	GAGAGTCGCC	GAGCCCATGG	60
CTTTCAGAGC	GACCCAGGC	CGGACGCCGC	CGGGACCCGG	ACCCAGATCC	GGAATCCCCCT	120
CAGCCAGCTT	CCCCAGCCCT	CAGCCCCCAA	TGGCGGGGCC	TGGAGGTATC	GAGGAAGAGG	180
ACGAGGAGGA	GCCC GCCGAG	ATCCATCTGT	CGGTGCTGTG	GAGCTCGGGA	TACCTGGGCA	240
TTGCTTACTA	TGACACTAGT	GACTCCACTA	TCCACTTCAT	GCCAGATGCC	CCAGACCACG	300
AGAGCCTAAA	GCTTCTCCAG	AGAGTTCTGG	ATGAAATCAA	CCCCCAGTCT	GTTGTCACAA	360
GTGCCAAACA	GGATGAGGCT	ATGACTCGAT	TTCTAGGGAA	GCTTGCCTCT	GAGGAGCACA	420
GAGAGCCAAA	GGGACCTGAA	ATCATACTTC	TGCCAAGCGT	GGATTTTGGT	CCAGAGATAA	480
GCAAACAGCG	TCTCCTTTCC	GGAAACTACT	CCTTCATCTC	AGACTCCATG	ACTGCTACTG	540

66221-92204159

AGAAAATCCT TTTCCTCTCC TCCATTATTC CCTTTGACTG TGTCCTCACG GTCCGGGCAC 600  
 TTGGAGGACT GCTCAAGTTC CTGAGTCGAA GAAGAATTGG GGTGAACTG GAAGACTATG 660  
 ATGTTGGCGT CCCTATCCTG GGATTCAAGA AGTTTGTATT GACCCATCTG GTGAGCATAG 720  
 ATCAAGACAC TTACAGCGTT CTACAGATTT TCAAGAGTGA GTCTCACCCC TCGGTGTACA 780  
 AAGTAGCCAG TGGGCTGAAG GAGGGGCTCA GCCTTTTTGG AATCCTCAAC AGATGCCGCT 840  
 GTAAGTGGGG ACAGAAGCTG CTCAGGCTGT GGTTTACACG TCCAACCCGG GAGCTAAGGG 900  
 AACTCAATTC CCGACTGGAT GTCATTCACT TCTTCCTGAT GCCTCAGAAC CTGGACATGG 960  
 CCCAGATGCT GCACCGACTC CTGAGCCACA TCAAGAATGT GCCTCTGATT CTGAAACGCA 1020  
 TGAAGTTGTC CCACACCAAG GTCAGTGAAT GGCAGGTCCT CTACAAGACT GTGTACAGTG 1080  
 CTCTCGGCCCT GAGGGATGCC TGCCGTTCTC TGCCACAGTC CATCCAGCTT TTTGAGGACA 1140  
 TTGCCCAGGA GTTCTCTGAC GACCTGCATC ACATTGCCAG CCTCATCGGG AAGGTGGTGG 1200  
 ACTTTGAGGA AAGTCTTGCT GAAAATCGCT TCACAGTCCT CCCTAACATA GACCCTGACA 1260  
 TAGATGCCAA GAAGCGAAGG CTGATAGGGC TTCCGAGCTT CCTCACTGAA GTTGCTCAGA 1320  
 AGGAGCTGGA GAACCTGGAC TCTCGCATCC CCTCATGCAG TGTCATCTAC ATCCCTCTGA 1380  
 TTGGCTTCCT TCTTTCCATT CCCCCTTGC CTTTCATGGT GGAAGCTAGT GACTTTGAGA 1440  
 TTGAGGGGCT GGAATTCATG TTTCTCTCAG AGGACAAGCT GCACTATCGT AGCGCCCGGA 1500  
 CCAAGGAGCT GGACACGCTG CTGGGAGACC TGCACTGTGA GATCCGGGAC CAGGAGACTC 1560  
 TGTGTATGTA CCAGCTGCAG TGCCAGGTGC TGGCACGGGC TTCGGTCTTG ACTCGGGTAT 1620  
 TGGACCTTGC CTCCCGCCTG GACGTCTTGT TGGCTCTTGC CAGTGCTGCC CGGGACTACG 1680  
 GCTATTCGAG ACCGCATTAC TCTCCCTGTA TCCATGGAGT ACGAATCAGG AATGGCAGGC 1740  
 ATCCTCTGAT GGAACCTGTG GCACGAACCT TCGTGCCCAA CTCCACGGAC TGTGGTGGGG 1800  
 ACCAGGGCAG GGTCAAAAGTC ATCACTGGAC CCAACTCCTC AGGGAAAAGC ATATATCTCA 1860  
 AGCAGGTAGG CTTGATCACT TTCATGGCCC TGGTGGGCAG TTTCGTGCCT GCAGAGGAGG 1920  
 CCGAGATTGG GGTAATCGAC GCCATCTTCA CTCGAATTCA CAGCTGCGAA TCCATCTCCC 1980  
 TCGGCCTCTC CACCTTCATG ATTGATCTCA ACCAGGTGGC GAAAGCAGTG AACAAATGCCA 2040  
 CAGAGCACTC GCTGGTCCTG ATCGATGAAT TCGGGAAGGG GACCAACTCG GTGGATGGCC 2100  
 TGGCACTTCT GGCTGCTGTG CTCCGCTACT GGCTTGCACT GGGACCCAGC TGCCCCCAGC 2160  
 TCTTTGTAGC CACCAACTTC CTGAGCCTTG TTCAGCTGCA GCTGCTGCCG CAAGGACCCC 2220  
 TGGTGAGTA TTGACCATG GAGACTTGTG AGGATGGGGA AGACCTTGTC TTCTTCTACC 2280  
 AGCTTTGCCA AGGCGTCGCC AGTGCCAGCC ACGCCTCCCA CACAGCGGCC CAGGCTGGGC 2340  
 TTCCTGACCC ACTCATTGCT CGTGGCAAAG AGGTCTCAGA CTTGATCCGC AGTGGGAAAC 2400  
 CCATCAAGGC CACGAATGAG CTTCTAAGGA GAAACCAAAT GGAAAACCTGC CAGGCACTGG 2460  
 TGGATAAGTT TCTAAACTG GACTTGGAGG ATCCCACCTT GGACCTGGAC ATTTTTCATTA 2520  
 GTCAGGAAGT GCTGCCCGCT GCTCCACCA TCCTCTGAGA GTCCTTCCAG TGTCCT 2576

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ala Phe Arg Ala Thr Pro Gly Arg Thr Pro Pro Gly Pro Gly Pro  
 1 5 10 15  
 Arg Ser Gly Ile Pro Ser Ala Ser Phe Pro Ser Pro Gln Pro Pro Met  
 20 25 30  
 Ala Gly Pro Gly Gly Ile Glu Glu Glu Asp Glu Glu Glu Pro Ala Glu  
 35 40 45  
 Ile His Leu Cys Val Leu Trp Ser Ser Gly Tyr Leu Gly Ile Ala Tyr

	50				55				60						
Tyr 65	Asp	Thr	Ser	Asp	Ser 70	Thr	Ile	His	Phe	Met 75	Pro	Asp	Ala	Pro	Asp 80
His	Glu	Ser	Leu	Lys 85	Leu	Leu	Gln	Arg	Val 90	Leu	Asp	Glu	Ile	Asn 95	Pro
Gln	Ser	Val	Val	Thr 100	Ser	Ala	Lys	Gln	Asp 105	Glu	Ala	Met	Thr 110	Arg	Phe
Leu	Gly	Lys	Leu	Ala 115	Ser	Glu	Glu	His	Arg 120	Glu	Pro	Lys	Gly 125	Pro	Glu
Ile	Ile	Leu	Leu	Pro	Ser	Val	Asp	Phe	Gly 130	Pro	Glu	Ile	Ser 135	Lys	Gln
Arg 145	Leu	Leu	Ser	Gly 150	Asn	Tyr	Ser	Phe	Ile 155	Ser	Asp	Ser	Met 160	Thr	Ala
Thr	Glu	Lys	Ile	Leu 165	Phe	Leu	Ser	Ser	Ile 170	Ile	Pro	Phe	Asp 175	Cys	Val
Leu	Thr	Val	Arg	Ala 180	Leu	Gly	Gly	Leu	Leu 185	Lys	Phe	Leu	Ser 190	Arg	Arg
Arg	Ile	Gly	Val	Glu 195	Leu	Glu	Asp	Tyr	Asp 200	Val	Gly	Val	Pro 205	Ile	Leu
Gly	Phe	Lys	Lys	Phe 210	Val	Leu	Thr	His	Leu 215	Val	Ser	Ile	Asp 220	Gln	Asp
Thr 225	Tyr	Ser	Val	Leu 230	Gln	Ile	Phe	Lys	Ser 235	Glu	Ser	His	Pro 240	Ser	Val
Tyr	Lys	Val	Ala	Ser 245	Gly	Leu	Lys	Glu	Gly 250	Leu	Ser	Leu	Phe 255	Gly	Ile
Leu	Asn	Arg	Cys	Arg 260	Cys	Lys	Trp	Gly	Gln 265	Lys	Leu	Leu	Arg 270	Leu	Trp
Phe	Thr	Arg	Pro	Thr 275	Arg	Glu	Leu	Arg	Glu 280	Leu	Asn	Ser	Arg 285	Leu	Asp
Val	Ile	Gln	Phe	Phe 290	Leu	Met	Pro	Gln	Asn 295	Leu	Asp	Met	Ala 300	Gln	Met
Leu 305	His	Arg	Leu	Leu 310	Ser	His	Ile	Lys	Asn 315	Val	Pro	Leu	Ile 320	Leu	Lys
Arg	Met	Lys	Leu	Ser 325	His	Thr	Lys	Val	Ser 330	Asp	Trp	Gln	Val 335	Leu	Tyr
Lys	Thr	Val	Tyr	Ser 340	Ala	Leu	Gly	Leu	Arg 345	Asp	Ala	Cys	Arg 350	Ser	Leu
Pro	Gln	Ser	Ile	Gln 355	Leu	Phe	Gln	Asp	Ile 360	Ala	Gln	Glu	Phe 365	Ser	Asp
Asp	Leu	His	His	Ile 370	Ala	Ser	Leu	Ile	Gly 375	Lys	Val	Val	Asp 380	Phe	Glu
Glu 385	Ser	Leu	Ala	Glu 390	Asn	Arg	Phe	Thr	Val 395	Leu	Pro	Asn	Ile 400	Asp	Pro
Asp	Ile	Asp	Ala	Lys 405	Lys	Arg	Arg	Leu	Ile 410	Gly	Leu	Pro	Ser 415	Phe	Leu
Thr	Glu	Val	Ala	Gln 420	Lys	Glu	Leu	Glu	Asn 425	Leu	Asp	Ser	Arg 430	Ile	Pro
Ser	Cys	Ser	Val	Ile 435	Tyr	Ile	Pro	Leu	Ile 440	Gly	Phe	Leu	Leu 445	Ser	Ile
Pro	Arg	Leu	Pro	Phe 450	Met	Val	Glu	Ala	Ser 455	Asp	Phe	Glu	Ile 460	Glu	Gly
Leu 465	Asp	Phe	Met	Phe 470	Leu	Ser	Glu	Asp	Lys 475	Leu	His	Tyr	Arg 480	Ser	Ala

Arg Thr Lys Glu Leu Asp Thr Leu Leu Gly Asp Leu His Cys Glu Ile  
 485 490 495  
 Arg Asp Gln Glu Thr Leu Leu Met Tyr Gln Leu Gln Cys Gln Val Leu  
 500 505 510  
 Ala Arg Ala Ser Val Leu Thr Arg Val Leu Asp Leu Ala Ser Arg Leu  
 515 520 525  
 Asp Val Leu Leu Ala Leu Ala Ser Ala Ala Arg Asp Tyr Gly Tyr Ser  
 530 535 540  
 Arg Pro His Tyr Ser Pro Cys Ile His Gly Val Arg Ile Arg Asn Gly  
 545 550 555 560  
 Arg His Pro Leu Met Glu Leu Cys Ala Arg Thr Phe Val Pro Asn Ser  
 565 570 575  
 Thr Asp Cys Gly Gly Asp Gln Gly Arg Val Lys Val Ile Thr Gly Pro  
 580 585 590  
 Asn Ser Ser Gly Lys Ser Ile Tyr Leu Lys Gln Val Gly Leu Ile Thr  
 595 600 605  
 Phe Met Ala Leu Val Gly Ser Phe Val Pro Ala Glu Glu Ala Glu Ile  
 610 615 620  
 Gly Val Ile Asp Ala Ile Phe Thr Arg Ile His Ser Cys Glu Ser Ile  
 625 630 635 640  
 Ser Leu Gly Leu Ser Thr Phe Met Ile Asp Leu Asn Gln Val Ala Lys  
 645 650 655  
 Ala Val Asn Asn Ala Thr Glu His Ser Leu Val Leu Ile Asp Glu Phe  
 660 665 670  
 Gly Lys Gly Thr Asn Ser Val Asp Gly Leu Ala Leu Leu Ala Ala Val  
 675 680 685  
 Leu Arg His Trp Leu Ala Leu Gly Pro Ser Cys Pro His Val Phe Val  
 690 695 700  
 Ala Thr Asn Phe Leu Ser Leu Val Gln Leu Gln Leu Leu Pro Gln Gly  
 705 710 715 720  
 Pro Leu Val Gln Tyr Leu Thr Met Glu Thr Cys Glu Asp Gly Glu Asp  
 725 730 735  
 Leu Val Phe Phe Tyr Gln Leu Cys Gln Gly Val Ala Ser Ala Ser His  
 740 745 750  
 Ala Ser His Thr Ala Ala Gln Ala Gly Leu Pro Asp Pro Leu Ile Ala  
 755 760 765  
 Arg Gly Lys Glu Val Ser Asp Leu Ile Arg Ser Gly Lys Pro Ile Lys  
 770 775 780  
 Ala Thr Asn Glu Leu Leu Arg Arg Asn Gln Met Glu Asn Cys Gln Ala  
 785 790 795 800  
 Leu Val Asp Lys Phe Leu Lys Leu Asp Leu Glu Asp Pro Thr Leu Asp  
 805 810 815  
 Leu Asp Ile Phe Ile Ser Gln Glu Val Leu Pro Ala Ala Pro Thr Ile  
 820 825 830  
 Leu

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GTAACCTCCG	CGTGACAGAA	TGAGGGTGGG	GCGCGTGGAG	TTTCCCACAA	TCTGTACTTT	60
AGTTAAATAC	CCGAGAATTC	ACCTCCTGTG	TCCACAGCTC	TCCACGCCCC	TCAGCCCTGC	120
CCCGCAGCCC	TGTATCAGAA	GTACTIONAGC	CTTTGCATTC	TGCGCGCCAC	CCTACCCCGG	180
CCTCCTCTGT	GAATCGTTGC	TTCCGAACCG	CCCTCACTTT	TTGCATCCGC	AG	232

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GTCTCTGAGG	GGAGTAGAAA	CTTGAATGGA	GAGTTGATGG	GAATTAAAA	TAAAAGAGGG	60
TTGGGAGCCG	GG//					74

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AAAAAAAAAC	AGGGTTGGGA	AGAGCTGGGC	AAGTCTCTTA	CCTCCTGAGT	GGCTGTTTCA	60
CATTCATAA	ATGGGGGTGA	TGATGCCTAT	CTCAGAGATT	TGAGAAAATG	ATTAAATTAT	120
ATAAGACATG	GTAAACCCTA	CATTATGAG	TGATTCTAAT	AGTGATTTC	TTTCTTCCTT	180
GCTGGACAG						189

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GTGGGGATGG	AACCATGAAT	TCCTCTGCTC	TCTGGGATTG	CAGATGTGTT	ACACACACAC	60
ACACACACAC	ACACACACAC	ACACACATAT	TTTTTTTTTC	TAGACAGAGT	CTTGCTCTGT	120

00470276-12299

(2) INFORMATION FOR SEO ID NO:59:

(A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GGCGACAAAT	ATATATGACG	TATTTACAAT	GTTTCAGGTG	CTTCAGATTC	AGCCCTGGGC	60
AAATCAGTCA	TGTCTGTTCT	CCAGGGGTTT	ACAGCCTAGT	GACAACATCC	AGAACATCCC	120
ACTTCCCTCT	CACCATCCCA	CCACTCTTAA	CTACTTTTCT	AAATCTCAAC	TTCTACCTGT	180
GTTCCCACTG	TGCAGAGCAC	TCCCTACTCC	TAGGGAGGAA	ATGTTTTTTGA	GAAGGAGAGG	240
GGTAGGAAGA	GGAGGGCTAT	GGGTTTTCTC	TTAGTCAAAG	ACAAAGATCC	TTTAACTCAT	300
TTGATCTCTG	TTCTCCTTCC	AAG				323

(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTAAGGACTT	GGTAAAGGAT	AGAGGGAAAA	TGGGGAAGGA	CTAATATATG	GAATATTCCA	60
GGGGGCTAGA	ATTGGGTGAG	AGGGAGTGTC	AGACAGAGGT	AGAAGGACTG	AGATGTAAAG	120
AATGATAGCC	TTTTCTTTCC	TCCCCACAG				150

(A) LENGTH: 733 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTATCTCCTT	CCTTTTGCTT	TGCCTAACTC	CCTGTTCCGG	TGTCCCATTG	TTTCCCCCAA	60
CTCTACCTTC	ATCATCACAG	ATCTCCCCCTC	TGCCTTATGT	CATCCTAAAC	CTTTGTGCTC	120

CTCATGCCCT	ATGACCTGTC	CCCCCAAGAT	CTCTCCTGCT	CCCTACCCTT	TAATAATCTG	180
CAGCTTATTG	GGAAGCCTCT	GCTTAAGTCA	TGTCTAGGGA	TGAGGGCCTC	CCCTGAGGAG	240
TGGTGACACT	TTTGGACAG	GGTTTATTG	TTGGAATTCT	CCCCATTAAG	TTAAAGCCTT	300
TTATCACCAA	ACCAAAAGGC	ACTGCCTCAG	TGACCCTTAT	TATGATCCAT	AAGGCACTTC	360
TATAACTTTC	CTAGGTTTAC	AATAAGAACA	GGAGTGTA	ATCCTAATTA	GATATTAAGG	420
CATTAGTGTT	ACTAGTTCTA	TTAATACCAT	TATTTTGACC	AAAATCCTCA	ATTCCAGACA	480
GATGTCTACT	TTCCTCAGCC	ATTTATCTTT	CTCAGGCTGT	GCTTTCAGAC	AAGTATCTTT	540
ATATTATATG	TAGAATAAAA	AGAGAATTAG	ACTAAGAGTC	TGAAAATTTG	GTTCTTGCTC	600
TAGCTTTCCA	TTAACTGCCT	GTGTGAGCTT	GGGCAAGTCA	AATAATCTCT	CTTGCTTCTA	660
TTGTCTCATT	CTTAAAATGG	GGTGAAAAAA	TTGAGCTACA	AGACCGTTCC	CTTTGCTTGC	720
CTCCCTCAAA	TAG					733

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GTGAGATTGG	TCCTGGGGGA	TAAGGGCTGG	GAGGCGGCAC	AAGTGCTAGG	GCTGAATTCT	60
GGGAGGTACT	GGCCTAGCCC	TGGAAAATAG	TAACTTTCCC	TGGTGCTCTG	CAGCCCCCAG	120
GAGATTTAAG	ATTTACCCCG	ATTCCACTGC	TGATCCCCTC	CCAG		164

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTAGGTGATT	CACCCCAACC	CCAACCAAG	TAATGTGGGA	TTGGGAGGCC	TGAAAAGTAA	60
AGTGGGGGTG	GGGTGTGGAT	GTGGCTGTGA	CCCAGTGGGT	CAAGGGCTCT	AGGACACCCG	120
GGAGAATCTA	AGGGCTAATG	AGACTTTGGG	AAGAAGACTG	GGACAATATT	CAGAGAGGGG	180
GACAAAGGAA	GTGGAGTTGT	GGAACGAAC	CAGACTGCTT	CCTGCTTTTT	TGTTTTCTGT	240
CCTCAG						246

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTAAAGAGGT	GGAGGCATGC	TGCTGTCTCT	GGGGAGGGAG	AAGGATTAAG	TTTAATGCCC	60
CAATAATCCT	AATGAGGCTC	TAGTTTCCCT	AATCCTGGGG	CTATTAAGAT	CTCTCTCCTT	120
GAAGGAAAGG	GAAGGGGGGT	TTTGAGGGAA	AGAGAGGAAG	AAAAGCATAA	AGATACTAGC	180
TTTCTTTTCT	ATAGGGAGAA	ACTGAGGCAA	AGAAAAGTAA	GGGACAAACC	TTACATCAAG	240
ATATGATCTC	GGCTGGGCGC	GGTGGCTCAT	GCCTGTAATC	CCCGCGCTTT	GGGAGGCCAA	300
GGCGGGTGGA	TCGCTGAGG	TCAGGAGTTT	GAGACCTGAC	CAATATGGTA	AAACCCCGTC	360
TCTACTAAAA	ATATAAAAT	TAGCTGGGTG	TGTTGTGCGC	CTGTAATCCC	A//	413

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTTTTTTTTTA	AAAAAAAAAA	AAAAAGACG	TGATCTCAGG	AGGATATCCC	CTGTCCCCAT	60
TCCATTTATC	AGTCTCAAT	TCTTATTTCC	CTCAAAAGTC	CAAGTTACCC	CAAACCTCCTC	120
CATTTCTCCT	CGACAG					136

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTAGGTGTGC	CCCATCCCTC	ATCTCACGTA	CAAAGACCTA	CCAGAAAAGC	AATTGGCTCC	60
AAAGATGTGT	CCCAGCCTCC	CTTCCCCTT	CACTCCCAT	GTCAGATATC	TCTTTCATGC	120
CAATCCAAAT	TTCTTACCTA	TTGTACCCC	CCGCCCCCA	AGCTTGAGCA	TCTTCCCATA	180
CTTTGTGGCT	GTACAGTGTG	TTGCATATCA	GCCATTACTT	TACCAATTCT	GTGTTCCCTC	240
CCTGGGTTTG	TATGAATGTT	TCTACTAGTT	GGGTACCTGT	TAGGGACTTT	GGGAGACCTT	300
GTGTATAGAG	AAGAGTTTTG	TAACTGCATA	ACTGCCTATT	TGATTTGTAT	AGAG//	356

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:



CCAGGAGTAG	AGGGAGAGAC	AGAAACAGCC	AACAATGGCC	CAGAAAATGG	ATGATATATT	60
AGATAAGGGA	AGAAATGAGT	TACCAGATTG	GGGAGAGATG	GTTTGGATGT	CAAAGCAGGT	120
GATCGGTGAC	GTCAGCGTCC	GAGGGAAGAC	GGCTGCCACC	GGCGGGGCCA	GTTGAGGGAA	180
CTAGGTAGTT	AAGTGTGTGC	GGGCTAAAAG	TCCCTAGAGT	GTCCATCCCT	CCCCATCTC	240
CATGTGCGGT	AATCCCAGCT	CATTTAGGGG	CCAGGCACCA	ACTTTGGTTG	CCTTTGTGCC	300
CTCCCAGGCC	AGCTTCCTCA	ACAACCAGCA	CCTCTGACTG	GATGCCTCAG	GTTAGACACA	360
TAAACACATT	CCATTGCCCT	GTCCGTGCCT	TGTAACAAGT	TCACTCCCTG	CCTTATCCCT	420
CACAAG						426

(2) INFORMATION FOR SEO ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTGAGTGGGT	CCCACACATA	CTACACACTA	ATGCATGAAT	TCCATATGCA	CACTACATAC	60
TAAGCCTACT	AATGCCAGTA	TACAGATTCT	CACATACACC	ACCCACCTA	GTAGTAGTAA	120
AGCAACTGCC	CTTACTGAG	CACTGGCTAA	CTGCATTTCA	TCCTTATAAC	AGCTTTGTGT	180
AGTAGCTGAT	ATGCATCTCA	TTTTTTGTTG	TCAGCGCAGG	TACACATATA	CATTGATGAT	240
ACACAGACTT	GCACATACAT	AGCAGCAGGA	AAAAACACAA	AATGTAAGGC	CGGGCAGAGT	300
GGCTCACACC	TGTTATCAGC	ACTTTGGGGG	GCCAACGCTG	GGTGACCTTC	CATCTTTG//	360

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CACAGGAAGA	ATATGAAAAG	ATGAATGTCT	GTTGCTGTTA	CCCAGAGACA	CTTTCACAGC	60
TAAAAAGACA	TACAAACTCA	TACTGACTCA	CCGTCTCTTA	CTCAGCCTCA	GAGTGAGCTG	120
CAGTGTGGC	ACACAAATAC	CTCAACACAC	TGCTCTCCTT	CTAAAATATT	GACAAGCTCC	180
GTTACTTATA	TACATGGAAT	GACACACGGT	CTTATCCGTT	GAAACTGTGA	TATGTAGACA	240
CAATTATGCT	CACATCTAGC	AATTTTCAGT	AGATACATGT	AAACACACCT	GAATGGGTAG	300
GACACTGCAC	TTGCCACTAC	ATTCCCATAG	CACATCGTGG	ATACATATTG	CCACAATCCC	360
CAGGGACTGC	AAGCAACACTT	TTTGGCAAAC	TGAGATCAAG	ATGATAGATG	TAAC TTGTAG	420
TACCCCCACC	CAAACCCTCA	CTTCCAG				447

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTGAGCCCAG	GGTGGAGGGC	AGGGAGGTGG	GGAAGGAGGT	TGAGGGCTGA	TACTGGGCAG	60
TGGGCTTCTT	GAGGGGCATT	AGAGTGAGGG	AAGAGAAAAC	AGCGGCTGTA	ACCTTGTCTG	120
ACTGTAG						127

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GTAAGGCCTT	CCTTCTTGAA	TCCCAAAA//	30
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(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TACAGGCATG	AGCCACTGTG	CCTGGCCAGG	ACCATATCTT	AATTGTCTTT	GTAGTTTCAG	60
TGTTTGGTAC	AGTGCCTCTC	ACTGTTTCTT	TTTGCCTTTG	AGATCTTCCC	TCTTTGTTAC	120
TGTGATCTTC	CCTACTGGTC	TTTGTCTCTC	TGAGTCTGTC	CCTATCACCA	CCTCAACCCG	180
AGCTGGATGT	GGCCTGTCCT	CCTTTTGTG	TTTCTCTCAC	AG		222

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTGAGTAGAA	GGAAAAAGGG	AGTGCACCCA	GGGAGGTCAG	GGAGAGAGAA	TGCAGTGTGC	60
AAGATGGGGA	AACATGGAAG	ATATTGAGGT	CAATTGGATA	AAGAATGGGA	TGGTGGGAGG	120
AGGCAGCAGA	ACTTCAGGGA	AGTATCTGGA	GGGTGAGAGT	TAAAGGAGGA	CTGCAGGGAG	180

AATTGGGGCC CAAGGAGAGC TGAGGAACAG GACAGAGGGT GCCAGGTCCT AAGAAACAGT 240  
 ACTTATCTCC TCAG 254

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTGAGTGTTG GGTGTGGATG GGCCTGTGAG CCTGCGCAG TGATGGAGTA CCATCCTTGG 60  
 CAGGTGGTCA CCACAGCTGG GGATCTTCAT AGCAACCAGG GCAGGAGACT CACTTTTGAT 120  
 AACCACCTGT CTTCCACCCT CGTAG 145

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GTGAGGGCAG GAGAGTGGGT GTAGCCTTCA GATGTCTTTT GGGGGAGATA TTAGGCTTAT 60  
 GAAAGACATA CTGGTAGATA AGAAAACTTG TGGGGC// 98

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATCTTTTAAG CTCCTTGGG ATGGGGAGGT TCCAGTAAGT CTCCAAACAA GAGAGTAGAG 60  
 TATCTCCTCT TACTCTCCC CAG 83

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

662221 92304460

(2) INFORMATION FOR SEQ ID NO:78:

(A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTGAGGAAAA	GCCAGAGGTT	ATATGCATTG	TAAGATGTTT	AAAAAAAGCA	GCAGCCAGGG	60
GAAGGAGGGG	AGTGGGCAAC	TTGGGGATGC	TTCCAACAGG	CCCCTCCTCT	TCCTGCTCTC	120
TGTCCTCGCTC	ACTCTGACTC	TATCTTTTCC	TCTGAATGTC	TTGAGGTCTC	AGATTGTATC	180
TGCAACCTGT	TTCCAGATCC	CCCTAGGGGC	CTCTGCCTCT	CCTTCACTTT	CCCCTGGAAC	240
TGACCTCCAG	CTCCCTTCCCT	CACCCATCC	CAG			273

(2) INFORMATION FOR SEO ID NO:79:

(A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:79:

GTAAGAATAG AGGCGGGTGG AGGAATACAC ATGAGGGGCC CAAAGGCTAC ATCTTCTGGG 60  
GGTTCATCTA TCTTGATCCA CAAGCCATGC GAGGTGCCTC TCCGCCCACT GCAG 114

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GTGAGGAGAA GCCCTGCAGC CTGGGCCTCT GCGGTCTCCT GCATCTACTC CACCCCTACT 60

TGCCAGCCAA	CTCAGGCTCC	TGCAGCTCTT	CTCCCATTTT	CTGACCCCGC	TCTTCATGAA	120
AGGACCATCA	CCCACATCCC	TGTGCTTCCA	CCTCACATGT	TCTTATFCTC	CACTGGAGAG	180
CCATGCTCTA	ATGGAACTTT	CCGTGGCCCA	AATTCCTTCA	CCTGCCTCTG	AGTAGGTACA	240
CACCACTCCC	AAGTATGTCT	CTGCCCACGT	CCCGTGCCTC	TTCCTGATT	CTAAATTAGC	300
CCACAGGGCT	ATGGTCAGGA	TTCGGGGAGG	AGAGACAGAG	TCAGTGTGTC	TGTTACCTAT	360
TTCTCCTGTT	TCACCCTGTC	CATTTCTCTT	TGATGTGCCA	TTCATGCCTT	GAGCCTCACT	420
TTCACCTCAG	CCCACGGCAC	CAGGCCCCAG	GCCCTGTCTC	CTTCCCTATT	CAG	473

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTCAAAGGGA	ACAAAGGGAG	GTGGGATTGA	GGAAGGGGAT	AATGGGAAAG	GAACCCCTGA	60
AAATGCTCAT	AACAGGAAAG	CATGCCCTCT	GCTGCATGCC	CTTTATACTA	AAAGTGGGGA	120
GCACTAAGGT	CAGAGATAAG	AAGAATCAAT	ACCATAAACA	TTTCTTGAAC	CCTTGTTTCA	180
TGTGAGTCAC	TGTTGGCAAA	GAGGATGAAC	AAAGCGTGCA	CCTCACCATT	CAAGAAGTTG	240
CAGTGCAGTA	GGGAGGGCAT	GTATACAGCT	TTATTCACAG	GCCAACTGTG	GTCAGTGCCT	300
TACGGGCTTC	CAATACTAAC	TTCCCCTTGT	CCACCTTATA	CCCAGCAG		348

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GTGAGGGGAG	AAACTGATGA	GGGGAGAAAC	TAAGGAGGGG	AAAATGGAGG	AGGATGAAGG	60
AGCATGACAG	TGAGGCTGGG	CCTCTGGAAT	GGAATAGGGC	TGTGTGGGCA	GAAAAGAAAT	120
AGAACACGAG	ACAGGGAAAG	GCAGTGCAAG	TGCAGAGGGG	CATATGGGGT	CCCCATGGCT	180
CCGAATGCTA	ACCTCTGCCC	TCTTTGCAG				209

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GTGAGGAGAC	CAATCTAGCT	CCTCGGGGAC	CCCCAGGCTG	GGCATTTCCT	AGAGGTGGGG	60
ATTGGCTCCT	CTATCAGAAC	AAGGGCTCCC	TCAGCACAGA	GACCACATCC	CTTCCCTTTT	120
CTCCCTCCCC	ACAGGATTGG	CCAAGGGTTT	CAGGACAGGA	AGGAGGTGAT	TGATGATACA	180
CTGTCTTTTA	TTCTCTTTTA	AG				202

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTGATGAGAT	CCAAATGTGC	AACCACCTCC	ACATCAGAGC	TCCCTTTCAT	TCCTAGTCCT	60
ACTGGGCCTG	GGTCTAGGTC	CACAGGATTT	CTGACCCTTA	TTTCCCCTTC	TCTTCCCCAC	120
TCCCCTTACT	CCTCCACCT	TCTTGCTTGT	CCTAG			155

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGCGTATAT	GGCCCCAGTG	TCTTTACCCT	CTCTGCATCT	TCTCCTGCAA	CTCTTCTCCC	60
CCCTCCAGCA	CTTTGCCCTT	CAGAAACCCA	CCATTTCTTT	CTGAAATCCC	TAAATCTTCA	120
AGATCCCAGG	TTTCTGTGTC	CACAGCCTCT	CCCCTCTGCC	CAGGGATTTG	GTGTGCCATT	180
CTGCCATAAA	TCTTGCGATT	TTCTCTCTTC	TTCAG			215

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCTGCTCAGG	TATACAGTAC	CACGCTCCC	29
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## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs

03470275-422299

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGATCCGGGG TGAGGAGCCC GTGGTAGGA

29

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAATGGCAGG TGAGAAGGGG CCCCATGTC

29

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTCAAGCAGG TGAGGGGCCG CCAAGCTGG

29

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ACCAACTCGG TGCGGAGGAA AATGAAGAG

29

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TTCCCATCCC AACCTCCAG GCTGTGGTT

29

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTCTCTCTCT CTTCTCCAG ACCAGGAGA

29

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGTCTCTCTA CCCACCACAG GCATCCTCT

29

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TCTCCCCTGC CCTGGCCCAG GTAGGCTTG

29

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

0547029-123



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCACCTCTGC CCTTTGACAG GTGGATGGC

29

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTATACAGTA CCACGCTCCC CAAGCAAAGT CAAGATGAGA GAAGACGTGA CTTGTAACCT  
TCCCATCCCA ACCCTCCAG

60

79

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTGAGGAGCC CGTGGTAGGA GGGGGCAGGC TGCTCTAACA GACCCTGCTC TCATGCTGGC  
CCCTCTGCAT GGTCACTG CATCTGCATG CCTGCTTCCA GATCTTTCCA GGCACCTCTC  
TCTCTCCTTC TCCAG

60

120

135

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGAGAAGGG GCCCATGTC CTGCTGTGGG GATCCTCCCT GGGTCCACAA ACCATGCAGT  
GTCTCTCTAC CCACCACAG

60

79

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGAGGGGCC	GCCAAGCTGG	GGGCCCACAT	CTCCATCTCC	TCTGGCCGCC	AGGCCAGATC	60
CTCTGCCCCC	CCCCACACAC	ACATACAGCA	CATGTCCTTG	TCCTCTGAGG	GACAGTCTGT	120
TCTTTAGGAT	AGACCTTTCC	GTGGCCACAA	GTCCCTGGAC	CAACCTCCAA	ATAGATCCAT	180
GCCGTTCCCT	AGTATGCCTT	TACCCACAAC	CTTGACTCTG	GAGTTAATTG	TGAAGTCAGG	240
ACCCAGGAAA	CTGTGTTCCA	GGGCTCTGTT	CTTCTGTTAC	ACTGTGTCCT	CTCTTTAATC	300
TGTCGTTTAT	GTCTTTAGTT	GAGACCCATT	TTTACTTTGC	CCATAGTACG	GCAACAGGCC	360
CATGTTCTGT	CTCCCCTGCC	CTGGCCCAG				389

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTGCGGAGGA	AAATGAAGAG	ATGCTAAGGA	GGGGGGATGG	AGGAAAATGA	GAACCGGGAG	60
CAGGAGACTG	ACCTCAGGGA	AGAAAAGGGG	GATGCGTGCA	CAGAGGGGAG	GAGAAGCCAT	120
GACAGCTACA	GAAGGACACA	GCTGTCCTGG	TTCTGCCCTC	TCACCTCTGC	CCTTTGACAG	180

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CCAGAACTCT	CTGGAGAAGC	20
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## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

65222T 9220460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTGCTGTGGA ATTCAGGATA C

21

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTCCACTATC CACTTCATGC CAGATGC

27

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GCTGGGGAGG AACTGGAAG GACTCTCA

28

652333T 940400